

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2003, 14:57:24 ; Search time 20 Seconds
(without alignments)
1490.615 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 310

Sequence: 1 MALRRPRLRLCARLPDFL.....VNYIRTDDEGDFRHKSFVI 310

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 9616862 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	2.6	290	2	168750	MHC class I lympho
2	8	2.6	336	2	A86406	Probable RING zinc
3	8	2.6	342	1	HLHUC4	MHC class I histoco
4	8	2.6	348	2	E82933	type I restriction
5	8	2.6	366	2	JH0546	class I histocompa
6	8	2.6	366	2	JH0547	class I histocompa
7	8	2.6	366	2	JH0545	class I histocompa
8	8	2.6	366	2	I37078	HLA-C alpha chain
9	8	2.6	492	2	AB1013	probable membrane
10	8	2.6	784	2	A86676	carbon starvation
11	7	2.3	77	2	JCS645	lymphotoxin beta -
12	7	2.3	113	2	AH1748	hypothetical prote
13	7	2.3	171	2	G70548	hypothetical prote
14	7	2.3	172	2	T08548	hypothetical prote
15	7	2.3	173	2	T01282	hypothetical prote
16	7	2.3	173	2	B90241	hypothetical prote
17	7	2.3	173	2	T25730	hypothetical prote
18	7	2.3	177	2	E85833	partial probable s
19	7	2.3	177	2	B90988	partial probable s
20	7	2.3	208	2	T03627	GRP-binding protei
21	7	2.3	208	2	T01588	GRP-binding protei
22	7	2.3	211	2	E86888	hypothetical prote
23	7	2.3	214	2	T47268	phosphatidylester
24	7	2.3	217	2	T10446	occlusion-derived
25	7	2.3	242	2	G84315	cobalt transport p
26	7	2.3	244	2	A46066	lymphotoxin beta
27	7	2.3	255	2	T35883	transcription regu
28	7	2.3	280	2	PH0269	epidermal autoanti
29	7	2.3	294	2	H84023	phosphate ABC tran

30	7	2.3	297	2	AB3037	hypothetical prote
31	7	2.3	297	2	A81002	conserved hypotnet
32	7	2.3	299	2	A98249	nutriate transport
33	7	2.3	300	2	A82017	probable lipoprote
34	7	2.3	302	2	B70471	heat shock protein
35	7	2.3	306	2	I49139	lymphotoxin-beta -
36	7	2.3	314	2	AG3093	hypothetical prote
37	7	2.3	314	2	C98193	sugar transport sy
38	7	2.3	324	2	T27302	hypothetical prote
39	7	2.3	333	2	I18974	G protein-coupled
40	7	2.3	343	2	H95879	probable sugar ABC
41	7	2.3	346	2	D75303	conserved hypotnet
42	7	2.3	362	2	G75614	GGERF family prote
43	7	2.3	375	2	T46378	hypothetical prote
44	7	2.3	376	2	F71815	hypothetical prote
45	7	2.3	380	2	E88421	hypothetical prote
46	7	2.3	382	2	T24963	protein R74.2 [imp
47	7	2.3	391	2	E72539	hypothetical prote
48	7	2.3	392	1	RWHUPD	hypothetical prote
49	7	2.3	392	2	B44194	poliovirus recepto
50	7	2.3	400	2	T24258	poliovirus recepto
51	7	2.3	402	2	T04348	endospore specific
52	7	2.3	402	2	G83367	hypothetical prote
53	7	2.3	403	1	GRECY	tyrosine-specific
54	7	2.3	403	2	G90955	tyrosine-specific
55	7	2.3	403	2	D85804	tyrosine-specific
56	7	2.3	417	1	RWHUPA	poliovirus recepto
57	7	2.3	417	2	A44194	poliovirus recepto
58	7	2.3	420	2	T16532	probable membrane
59	7	2.3	421	2	H86217	protein T2767.16 (
60	7	2.3	431	2	D81282	probable efflux pr
61	7	2.3	437	2	AE1849	proton/sodium-glut
62	7	2.3	454	2	JC4616	aprase (EC 3.6.1.
63	7	2.3	463	2	D84065	glucose-1-phosphat
64	7	2.3	481	2	S69808	lincomycin resist
65	7	2.3	490	2	A66556	probable tRNA-guan
66	7	2.3	490	1	QARBPC	cytochrome P450 2B
67	7	2.3	491	2	S31277	cytochrome P450 2B
68	7	2.3	491	2	S31278	cytochrome P450 2B
69	7	2.3	491	2	S35666	cytochrome P450 2B
70	7	2.3	503	2	B83490	probable MFS trans
71	7	2.3	504	2	B87628	hypothetical prote
72	7	2.3	523	2	B95922	hypothetical nucle
73	7	2.3	524	2	A31318	glucose transport
74	7	2.3	530	2	C95268	probable ABC trans
75	7	2.3	558	2	B87098	conserved hypotnet
76	7	2.3	558	2	G70879	hypothetical prote
77	7	2.3	595	2	H69345	translation initia
78	7	2.3	618	2	A36907	pyocin S1 S1A subu
79	7	2.3	629	2	AD1838	Na+/H+ antiporter
80	7	2.3	643	2	A41120	prostaglandin tran
81	7	2.3	671	2	PH0268	epidermal autoanti
82	7	2.3	688	2	H83070	conserved hypotnet
83	7	2.3	689	2	D83501	pyocin S2 PA150 (
84	7	2.3	690	2	C36907	pyocin S2 S2A subu
85	7	2.3	693	1	S38427	NADPH-ferrithomop
86	7	2.3	698	1	A47203	protein-glutamine
87	7	2.3	705	2	T16088	hypothetical prote
88	7	2.3	709	2	C67258	fatty oxidation co
89	7	2.3	716	2	AB1070	probable carbon st
90	7	2.3	721	2	S56580	carbon starvation
91	7	2.3	721	2	A98293	probable carbon st
92	7	2.3	721	2	D66134	probable carbon st
93	7	2.3	741	2	H90607	atp-dependent heli
94	7	2.3	747	2	T40728	hypothetical prote
95	7	2.3	758	1	S45477	SEC18 protein - ye
96	7	2.3	780	2	T29580	hypothetical prote
97	7	2.3	788	2	T44262	transducer (Htr6
98	7	2.3	798	2	E84236	transducer (Htr6
99	7	2.3	798	2	T48304	hypothetical prote
100	7	2.3	815	2	H96494	protein F7F22.2 (I

ALIGNMENTS

RESULT 1

MHC class I lymphocyte antigen - human (fragment)
A:Accession: A24512
A:Molecule type: DNA
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
C:Accession: 168750
R:Polha, H.; Kwon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B
A:Reference number: 154457; MUID:89233295; PMID:2714852
A:Accession: 168750
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-290 <RES>
A:Cross-references: GB:M28207; NID:9576478; PIDN:AAA53259.1; PID:9576479
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:144-209/Domain: immunoglobulin homology <IMM>

Query Match

2.6%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 LVVLAVL 256
|||||
Db 241 LVVLAVL 248

RESULT 2

probable RING zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A86406
R:Phellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 815-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzigberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86441; MUID:21016719; PMID:11130712
A:Accession: A86406
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <STO>
A:Cross-references: GB:AE005172; NID:911024872; PIDN:AA626956.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match

2.6%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVL 257
|||||
Db 28 LVVLAVL 35

RESULT 3

HLHUC4
MHC class I histocompatibility antigen HLA-C4 alpha chain - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C:Accession: A24512
R:Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
A:title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonucleotide

A:Reference number: A92500; MUID:86033791; PMID:3863816

A:Accession: A24512

A:Molecule type: DNA

A:Residues: 1-342 <DAV>

A:Cross-references: GB:M11886; NID:9184173; PIDN:AAA52665.1; PID:9386777

C:Genetics:

A:Gene: GDB:HLA-C

A:Cross-references: GDB:119311; OMIM:142840

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

F:196-261/Domain: immunoglobulin homology <IMM>

F:66/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

2.6%; Score 8; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 LVVLAVL 256
|||||
Db 293 LVVLAVL 300

RESULT 4

type I restriction enzyme M protein, truncated homolog UU098 [imported] - Ureaplasma ure
E82933
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Oct-2002
C:Accession: E82933
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to Genbank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: E82933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <GLA>
A:Cross-references: GB:AE002110; GB:AF222894; NID:96899051; PIDN:AAF30504.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: hsdM-1; UU098
A:Genetic code: SGC3
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match

2.6%; Score 8; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 RKEIDELV 130
|||||
Db 336 RKEIDELV 343

RESULT 5

JH0546
class I histocompatibility antigen Gogo-CO202 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0546
R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A:title: Gorilla class I major histocompatibility complex alleles: comparison to human A
A:Reference number: JH0534; MUID:92078860; PMID:1744581
A:Accession: JH0546
A:Molecule type: DNA
A:Residues: 1-366 <LAW>
A:Cross-references: EMBL:X60249; NID:922882; PIDN:CAA42801.1; PID:922883
A:Experimental source: EBV-transformed B cell
C:Genetics:
A:Introns: 25/1, 115/1, 207/1, 299/1, 339/1, 350/1, 366/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0202 #status pre
F:25-114/Domain: alpha-1 <AL1>
F:115-206/Domain: alpha-2 <AL2>
F:207-298/Domain: alpha-3 <AL3>
F:220-285/Domain: immunoglobulin homology <IMM>
F:299-366/Domain: intracellular #status predicted <INT>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 249 VLWVLA VL 256
DB 317 VLWVLA VL 324

RESULT 6

JH0547
class I histocompatibility antigen Gogo-C0203 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0547

R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991

A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A:Reference number: JH0534; MUID:92078860; PMID:1744581

A:Accession: JH0547

A:Molecule type: DNA

A:Residues: 1-366 <LAW>
A:Cross-references: EMBL:X60248; NID:G22884; PIDN:CAA42800.1; PID:G22885

A:Experimental source: EBV-transformed B cell

C:Genetics:
A:Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0203 #status pre

F:25-114/Domain: alpha-1 <AL1>
F:115-206/Domain: alpha-2 <AL2>
F:207-298/Domain: alpha-3 <AL3>
F:220-285/Domain: immunoglobulin homology <IMM>
F:299-366/Domain: intracellular #status predicted <INT>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 249 VLWVLA VL 256
DB 317 VLWVLA VL 324

RESULT 7

JH0545
class I histocompatibility antigen Gogo-C0201 heavy chain precursor - lowland gorilla
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: JH0545

R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991

A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A:Reference number: JH0534; MUID:92078860; PMID:1744581

A:Accession: JH0545

A:Molecule type: DNA

A:Residues: 1-366 <LAW>
A:Cross-references: EMBL:X60251; NID:G22880; PIDN:CAA42803.1; PID:G22881

A:Experimental source: EBV-transformed B cell

C:Genetics:
A:Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0201 #status pre

F:25-114/Domain: alpha-1 <AL1>
F:115-206/Domain: alpha-2 <AL2>
F:207-298/Domain: alpha-3 <AL3>
F:220-285/Domain: immunoglobulin homology <IMM>
F:299-366/Domain: intracellular #status predicted <INT>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 249 VLWVLA VL 256
DB 317 VLWVLA VL 324

RESULT 8

H37078
HLA-C alpha chain - human

C:Species: Homo sapiens (man)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: H37078

R:Vilches, C.; Bunce, M.; de Pablo, R.; Herrero, M.J.; Kreisler, M.
Tissue Antigens 46, 19-23, 1995

A:Title: Anchored PCR cloning of the novel HLA-Cw*0704 allele detected by PCR-SSP.
A:Reference number: H37078; MUID:96086482; PMID:7482492

A:Accession: H37078

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-366 <RES>
A:Cross-references: EMBL:X83394; NID:G669131; PIDN:CAA58333.1; PID:G669132

C:Genetics:
A:Gene: Cw*0704

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 249 VLWVLA VL 256
DB 317 VLWVLA VL 324

RESULT 9

AB1013
probable membrane protein STY4415 [imported] - Salmonella enterica subsp. enterica serov.

C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AB1013

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.

Nature 413, 848-852, 2001
A:Author: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov.

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-492 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAN09203.1; PID:G16505207; GSPDB:GN00176

C:Genetics:
A:Gene: STY4415

Query Match 2.6%; Score 8; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 242 IGGITGV 249
DB 244 IGGITGV 251

RESULT 10

A:Accession: A86676
C:Species: Lactococcus lactis subsp. lactis (strain IL1403)
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
R:Polonin, A.; Winkler, P.; Mauger, S.; Jallou, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp.
A/Reference number: A86625; MUID:21235166; PMID:11337471
A/Accession: A86676
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-784 <STO>
A/Cross-references: GB:AE005176; PID:g12723283; PIDN:AAK04507.1; GSPDB:GN00146
A/Experimental source: strain IL1403
A/Genetics:
A/Gene: catA
C:Superfamily: carbon starvation protein

Query Match 2.3%; Score 7; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLAVLALI 259
DB 223 VLAVLALI 230

RESULT 11

JC5645
A:Accession: JC5645
C:Species: Homo sapiens (man)
C/Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 05-Nov-1999
R:Marzocchi, K.; Renard, N.; Charlot, C.; Bienvenu, J.; Collier, B.; Salles, G.
Biochem. Biophys. Res. Commun. 238, 273-276, 1997
A/Title: Identification of two lymphotoxin beta isoforms expressed in human lymphoid cell
A/Reference number: JC5645; MUID:97445965; PMID:9299492
A/Accession: JC5645
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-77 <MAR>
A/Cross-references: GB:U89922; NID:g1870795; PIDN:AAC51769.1; PID:g1870796
C/Comment: This protein is involved in the development and function of the immune system

Query Match 2.3%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLAVLALI 258
DB 40 VLAVLALI 46

RESULT 12

AH1748
A:Accession: AH1748
C:Species: Listeria innocua (strain C11p11262)
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
R:Daaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fahl, H.
Science 294, 849-852, 2001
A:Authors: Kieft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlieter, I.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AH1748

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-113 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC97760.1; PID:g16415055; GSPDB:GN00178
A/Experimental source: strain C11p11262
C/Genetics:
A/Gene: 11n2533

Query Match 2.3%; Score 7; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 GGIGGV 249
DB 15 GGIGGV 21

RESULT 13

G70548
A:Accession: G70548
C:Species: Mycobacterium tuberculosis (strain H37RV)
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
R/Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: G70548
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-171 <COU>
A/Cross-references: GB:Z95558; GB:AL123456; NID:g3261781; PIDN:CAB08967.1; PID:e316801;
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV0556
C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0556

Query Match 2.3%; Score 7; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVL 256
DB 150 LVVLAVL 156

RESULT 14

T08548
A:Accession: T08548
C:Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
R:Bevan, M.; Zimmermann, W.; Gruenewald, A.; Wamboldt, R.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16442
A/Accession: T08548
A/Molecule type: DNA
A/Residues: 1-172 <BEV>
A/Cross-references: EMBL:AL050352; GSPDB:GN00062; ATSP:F27B13.110
A/Experimental source: cultivar Columbia; BAC clone F27B13
C/Genetics:
A/Gene: ATSP:F27B13.110
A/Map position: 4

Query Match 2.3%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPRRLRL 11
|||||||

Db 37 RPPRLRL 43

RESULT 15

hypothetical protein At2g19340 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F27F23.14
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C:Accession: T01282; E84575
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.
A:Reference number: 214177
A:Accession: T01282
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-173 <R0U>
A:Cross-references: EMBL:AC003058; NID:g3135250; PID:g3135264
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayan, L.; Talion, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-173 <STO>
A:Cross-references: GB:AE002093; NID:g3135264; PIDN:AAIC6464.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g19340; F27F23.14
A:Map position: 2

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 173;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPPRLRL 11
|||||
Db 38 RPPRLRL 44

RESULT 16

hypothetical protein SS00903 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: B90241
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A39139
A:Accession: B90241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-173 <KUR>
A:Cross-references: GB:AE006641; NID:g13814083; PIDN:AAK41185.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS00903

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 173;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 IIGGVLV 251
|||||
Db 102 IIGGVLV 108

RESULT 17

hypothetical protein F25B4.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25730
R:Gattung, S.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid F25B4.
A:Reference number: 220076
A:Accession: T25730
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-173 <GAT>
A:Cross-references: EMBL:U64842; PIDN:AAB37085.1; GSPDB:GN00023; CESP:F25B4.9
A:Experimental source: strain Bristol N2; clone F25B4
C:Genetics:
A:Gene: CESP:F25B4.9
A:Map position: 5
A:Introns: 17/1; 42/2; 147/3

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 173;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 VVALITL 261
|||||
Db 2 VVALITL 8

RESULT 18

partial probable sensor kinase Z3235 [imported] - Escherichia coli (strain O157:H7, sube
E85833
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85833
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamouis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85833
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <STO>
A:Cross-references: GB:AE005174; NID:g12516269; PIDN:AA657129.1; GSPDB:GN00145; UMGF:Z32
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3235

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 177;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 GGVLVVL 253
|||||
Db 139 GGVLVVL 145

RESULT 19

partial probable sensor kinase E6e2874 [similarity] - Escherichia coli (strain O157:H7,
B90988
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: B90988
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A96629; MUID:21156231; PMID:11258796
A:Accession: B90988
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-177 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA36297.1; PID:g3362343; GSPDB:GN00154
 A:Experimental source: strain 0157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: EC52874

Query Match 2.3%; Score 7; DB 2; Length 177;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 GGVLYVL 253
 |||||
 DB 139 GGVLYVL 145

RESULT 20
 T03627
 GTP-binding protein Rab6 - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
 C:Accession: T03627
 R:Haizel, T.; Merkle, T.; Turk, F.; Nagy, F.
 Plant Physiol. 108, 59-67, 1995
 A:Title: Characterization of membrane-bound small GTP-binding proteins from Nicotiana ta
 A:Reference number: Z14896; MUID:95303981; PMID:7784525
 A:Accession: T03627
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-208 <HAI>
 A:Cross-references: EMBL:I29273; NID:g623585; PIDN:AAA74117.1; PID:g623586
 A:Experimental source: strain SRI
 C:Genetics:
 A:Gene: Rab6
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keyword: GTP binding; membrane trafficking; nucleotide binding; P-loop
 F:10-125/Domain: translation elongation factor Tu homology <ETU>
 F:16-23/Region: nucleotide-binding motif A (P-loop)
 F:122-125/Region: GTP-binding NKXD motif
 F:152-154/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 VNLKSSN 38
 |||||
 DB 187 VNLKSSN 193

RESULT 21
 T01588
 GTP-binding protein Atg344610 - Arabidopsis thaliana
 N:Alternate names: protein F16B22.10
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Mar-2001
 C:Accession: T01588; F84880
 R:Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, July 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.
 A:Reference number: Z14284
 A:Accession: T01588
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1208 <ROU>
 A:Cross-references: EMBL:AC003672; NID:g3341671; PIDN:AAC27463.1; PID:g3341681
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 Neuse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: AB84420; MUID:20083487; PMID:10617197
 A:Accession: F84880

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-208 <STO>
 A:Cross-references: GB:AE002093; NID:g3341681; PIDN:AAC27463.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: F16B22.10; Atg344610
 A:Map position: 2
 A:Introns: 39/3; 63/2; 93/1; 130/2; 160/3
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
 F:10-125/Domain: translation elongation factor Tu homology <ETU>
 F:16-23/Region: nucleotide-binding motif A (P-loop)
 F:122-125/Region: GTP-binding NKXD motif
 F:152-154/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 VNLKSSN 38
 |||||
 DB 187 VNLKSSN 193

RESULT 22
 E86888
 hypothetical protein y1A [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: E86888
 R:Boltin, A.; Winkler, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A:Reference number: AB6625; MUID:21235186; PMID:11337471
 A:Accession: E86888
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-211 <STO>
 A:Cross-references: GB:AE005176; PID:g12725164; PIDN:AAK06207.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: y1A

Query Match 2.3%; Score 7; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 GGIIGCV 249
 |||||
 DB 45 GGIIGCV 51

RESULT 23
 T47268
 phosphatidylserine synthase [imported] - Helicobacter felis
 C:Species: Helicobacter felis
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
 C:Accession: T47268
 R:Bayle, D.; Wangler, S.; Weltzenegger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.; S
 J. Bacteriol. 180, 317-329, 1998
 A:Title: Properties of the P-type ATPases encoded by the copA operons of Helicobacter p
 A:Reference number: Z24437; MUID:98101471; PMID:9440521
 A:Accession: T47268
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-214 <BAY>
 A:Cross-references: EMBL:AJ001932; NID:g2660538; PIDN:CAA05103.1; PID:g2660541
 A:Experimental source: strain ATCC 49179
 C:Superfamily: Bacillus subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase; Bac
 F:9-16/Domain: Bacillus subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase hor

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 FFLLLF 24
 |||||
 Db 172 FFLLLF 178

RESULT 24

T30446

occlusion-derived virus envelope protein odv-e25 - *lymantiria dispar* nuclear polyhedrosis
 C:Species: *lymantiria dispar* nuclear polyhedrosis virus, LdMNPV
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T30446
 R:Kurio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
 virology 253, 17-34, 1999
 A>Title: Sequence and analysis of the genome of a baculovirus pathogenic for *lymantiria*
 A:Reference number: Z20836; MUID:99124785; PMID:9887315
 A:Accession: T30446
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-217 <KUZ>
 A:Cross-references: EMBL:AF081810; NID:G3822234; PIDN:AAC70282.1; PID:G3822331
 C:Keywords: envelope protein

Query Match 2.3%; Score 7; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVL 256
 |||||
 Db 9 LVVLAVL 15

RESULT 25

G84315

cobalt transport protein [imported] - *Halobacterium* sp. NRC-1
 C:Species: *Halobacterium* sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84315
 R:Ng, W.V.; Kennedy, S.P.; Mahataas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
 ; Leithauser, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Jung, K.H.; Alam, M.; Freilais, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
 A>Title: Genome sequence of *Halobacterium* species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: G84315
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-242 <STO>
 A:Cross-references: GB:AE004437; NID:G10581105; PIDN:AAG19891.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: cb1Q

Query Match 2.3%; Score 7; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 VLVVLAV 255
 |||||
 Db 231 VLVVLAV 237

RESULT 26

A46066

lymphotoxin beta - human
 C:Species: *Homo sapiens* (man)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A46066
 R:Browning, J.L.; Ngam-ek, A.; Lawton, P.; DeMarinis, J.; Tizard, R.; Chow, E.P.; Hesse
 Ceil 72, 847-855, 1993
 A>Title: Lymphotoxin beta, a novel member of the TNF family that forms a heteromeric com
 A:Reference number: A46066; MUID:93208881; PMID:7916655

A:Accession: A46066
 A:Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-244 <BRO>
 A:Cross-references: GB:L11015; NID:G292276; PIDN:AAA36191.1; PID:G292277
 A>Note: sequence extracted from NCBI backbone (NCBIN:128066, NCBI:P:128067)
 C:Keywords: transmembrane protein

Query Match 2.3%; Score 7; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 VLVVLAV 258
 |||||
 Db 40 VLVVLAV 46

RESULT 27

T35883

transcription regulator - *Streptomyces coelicolor*
 C:Species: *Streptomyces coelicolor*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: T35883
 R:Olliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, November 1997
 A:Reference number: Z21592
 A:Accession: T35883
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-255 <OLT>
 A:Cross-references: EMBL:AL009204; PIDN:CAA15804.1; GSPDB:GN00070; SCOEDB:SC9B10.14
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC9B10.14
 C:Superfamily: transcription regulator GntR

Query Match 2.3%; Score 7; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 IELTVQV 137
 |||||
 Db 233 IELTVQV 239

RESULT 28

PH0269

epidermal autoantigen 450K (clone pE450-B) - human (fragment)
 C:Species: *Homo sapiens* (man)
 C:Date: 25-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Oct-1997
 C:Accession: PH0269
 R:Fujitawa, S.; Kohno, K.; Iwamatsu, A.; Naio, I.; Shinkai, H.
 submitted to JIPID, July 1995
 A:Description: The 450kD epidermal autoantigen is a novel protein in plectin family.
 A:Reference number: PH0269
 A:Accession: PH0269
 A:Molecule type: mRNA
 A:Residues: 1-280 <FTU>
 C:Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S

Query Match 2.3%; Score 7; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 AYRGYF 272
 |||||
 Db 204 AYRGYF 210

RESULT 29

H64033

phosphate ABC transporter (permease) BH2992 [imported] - *Bacillus halodurans* (strain C-1
 C:Species: *Bacillus halodurans*

C:/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:/Accession: H84023
R./Takemi, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A./Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A./Reference number: AB3650; PMID:20512582; PMID:11058132
A./Accession: H84023
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-294 <STO>
A./Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06711.1; GSPDB:GN00
A./Experimental source: strain C-125
C./Genetics:
A./Gene: BH2992
C./Superfamily: phoW protein

Query Match 2.3%; Score 7; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVL 256
|||||
DB 35 LVVLAVL 41

RESULT 30
AB3037
hypothetical protein nrtB [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C./Species: *Agrobacterium tumefaciens*
C./Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C./Accession: AB3037
R./Wood, D.W.; Sebubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erge, G.; Gillier, W.; Grant, C.; Guenther, D.; Kutyavln, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A./Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A./Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A./Reference number: AB2577; PMID:21608550; PMID:11743193
A./Accession: AB3037
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-297 <KUR>
A./Cross-references: GB:AE008689; PIDN:AA44712.1; PID:g17742343; GSPDB:GN00187
A./Experimental source: strain C58 (Dupont)
C./Genetics:
A./Gene: nrtB
A./Map position: linear chromosome
C./Superfamily: *Synechococcus* nitrate transport protein nrtB

Query Match 2.3%; Score 7; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVL 256
|||||
DB 50 LVVLAVL 56

RESULT 31
AB1002
conserved hypothetical protein NMB2139 [imported] - *Neisseria meningitidis* (strain MC58
C./Species: *Neisseria meningitidis*
C./Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C./Accession: AB1002
R./Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Masegiani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A./Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A./Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A./Reference number: AB1000; PMID:20157555; PMID:10710307
A./Accession: AB1002

A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-297 <TER>
A./Cross-references: GB:AE002562; GB:AE002098; NID:g7227392; PIDN:AA42447.1; PID:g722739
A./Experimental source: serogroup B, strain MC58
C./Genetics:
A./Gene: NMB2139

Query Match 2.3%; Score 7; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 AEILGKT 98
|||||
DB 100 AEILGKT 106

RESULT 32
A98249
nitrate transport permease protein nrtB AGR_L_1888 [imported] - *Agrobacterium tumefaciens*
C./Species: *Agrobacterium tumefaciens*
C./Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C./Accession: A98249
R./Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A./Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A./Reference number: A97359; PMID:21608551; PMID:11743194
A./Accession: A98249
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-299 <KUR>
A./Cross-references: GB:AE007870; PIDN:AAK89515.1; PID:g15159391; GSPDB:GN00170
C./Genetics:
A./Gene: AGR_L_1888
A./Map position: linear chromosome
C./Superfamily: *Synechococcus* nitrate transport protein nrtB

Query Match 2.3%; Score 7; DB 2; Length 299;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 LVVLAVL 256
|||||
DB 52 LVVLAVL 58

RESULT 33
AB2017
probable lipoprotein NMA0225 [imported] - *Neisseria meningitidis* (strain Z2491) roup
C./Species: *Neisseria meningitidis*
C./Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C./Accession: AB2017
R./Fairhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A./Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A./Reference number: AB1775; PMID:20222556; PMID:10761919
A./Accession: AB2017
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-300 <PAR>
A./Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83536.1; PID:g737899
A./Experimental source: serogroup A, strain Z2491
C./Genetics:
A./Gene: NMA0225

Query Match 2.3%; Score 7; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 AEILGKT 98
|||||

Db 103 AELLGKT 109

RESULT 34

B70471
heat shock protein X - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Aug-1999
C:Accession: B70471
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-359, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: B70471
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-302 <AGP>
A:Cross-references: GB:AE000766; NID:92984216; PIDN:AA07747.1; PID:92984218; GB:AE00065
A:Experimental source: strain VFS
C:Genetics:
A:Gene: htpX
C:Superfamily: heat-shock protein htpX

Query Match 2.3%; Score 7; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 242 IGGIIGG 248
Db 31 IGGIIGG 37

RESULT 35

I49139
lymphotoxin-beta - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49139; I49138; I49076
R:Latton, P.; Nelson, J.; Tizard, R.; Browning, J.L.
J. Immunol. 154, 239-246, 1995
A:Title: Characterization of the mouse lymphotoxin-beta gene.
A:Reference number: I49138; MUID:95088371; PMID:7995944
A:Accession: I49139
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-306 <RES>
A:Cross-references: EMBL:U16985; NID:9577830; PIDN:AA70089.1; PID:9577831
A:Accession: I49138
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-306 <RES>
A:Cross-references: EMBL:U16984; NID:9577431; PIDN:AA60493.1; PID:9577432
R:Pokholok, D.K.; Maroulakou, I.G.; Kupriash, D.V.; Alimhanov, M.B.; Kozlov, S.V.; Novot
Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995
A:Title: Cloning and expression analysis of the murine lymphotoxin beta gene.
A:Reference number: A55602; MUID:95148600; PMID:7846035
A:Accession: I49076
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <RE2>
A:Cross-references: EMBL:U12029; NID:9515508; PIDN:AA67716.1; PID:9515509
C:Genetics:
A:Gene: LT-beta
A:Introns: 54/3; 160/1

Query Match 2.3%; Score 7; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 252 LVAVLAVL 258
Db 40 LVAVLAVL 46

RESULT 36

AG3093
hypothetical protein Atu4371 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AG3093
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ser, B.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG3093
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <KUR>
A:Cross-references: GB:AE008689; PIDN:AA45165.1; PID:917742841; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4371
A:Map position: linear chromosome
C:Superfamily: l-arabinose transport system permease araH

Query Match 2.3%; Score 7; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 250 LVAVLAVL 256
Db 16 LVAVLAVL 22

RESULT 37

C98193
sugar transport system permease protein homolog (AF036920) [imported] - Agrobacterium tum
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: C98193
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: C98193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK89069.1; PID:91515867; GSPDB:GN00170
C:Genetics:
A:Gene: AGR L 991
A:Map position: linear chromosome
C:Superfamily: l-arabinose transport system permease araH

Query Match 2.3%; Score 7; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 250 LVAVLAVL 256
Db 16 LVAVLAVL 22

RESULT 38

T27302
hypothetical protein Y68A4.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27302
R:Steward, C.

submitted to the EMBL Data Library, January 1998
A:Reference number: Z20340
A:Accession: T27302
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <WIL>
A:Cross-references: EMBL:AL021503; PIDN:CAA16423.1; GSPDB:GN00023; CESP:Y68A4A.6
A:Experimental source: clone Y68A4A
C:Genetics:
A:Gene: CESP:Y68A4A.6
A:Map position: 5
A:introns: 48/3; 88/2; 187/3; 242/3

Query Match
Best Local Similarity 2.3%; Score 7; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 FULLFR 25
|||
Db 235 FULLFR 241

RESULT 39
138974
G:protein-coupled receptor 8 - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
C:Accession: I38974
R:O'Dowd, B.F.; Scheidegger, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
Genomics 28, 84-91, 1995
A:Title: The cloning and chromosomal mapping of two novel human opioid-somatomostatin-like
A:Reference number: A57647; MUID:96070436; PMID:7590751
A:Accession: I38974
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-333 <RES>
A:Cross-references: EMBL:U22492; NID:g953234; PIDN:AAC50198.1; PID:g953235
C:Genetics:
A:Gene: GDB:GPR8
A:Cross-references: GDB:371716; OMIM:600730
A:Map position: 20q13.3-20q13.3
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match
Best Local Similarity 2.3%; Score 7; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 VLVVLAV 255
|||
Db 262 VLVVLAV 268

RESULT 40
H95879
probable sugar ABC transporter permease protein SMB20318 [imported] - *Sinorhizobium meli*
C:Species: *Sinorhizobium meli*
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: H95879
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb *psymb* megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:2136508; PMID:11481431
A:Accession: H95879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-343 <KUR>
A:Cross-references: GB:AL591985; PIDN:CA048704.1; PID:g15140177; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid *psymb*
R:Galibert, F.; Finan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaute, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meli*
A:Reference number: A86039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB20318
A:Genome: plasmid
C:Superfamily: l-arabinose transport system permease arax

Query Match
Best Local Similarity 2.3%; Score 7; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 GVLVLA 254
|||
Db 73 GVLVLA 79

RESULT 41
D75303
Conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75303
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75303
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-346 <WHI>
A:Cross-references: GB:AE002053; GB:AE000513; NID:96459999; PIDN:AAF11754.1; PID:9646000
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2205
A:Map position: 1

Query Match
Best Local Similarity 2.3%; Score 7; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 GVLVLA 254
|||
Db 333 GVLVLA 339

RESULT 42
G75614
GGDEF family protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: G75614
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75614
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <WHI>
A:Cross-references: GB:AE001862; GB:AE001825; NID:96460468; PIDN:AAF12191.1; PID:9646048
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0181
A:Map position: 2

Query Match
Best Local Similarity 2.3%; Score 7; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 257 ALITIGI 263
Db 178 ALITIGI 184

RESULT 43

T6378
hypothetical protein DKFZp434G0719.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C/Accession: T6378
R/Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A/Reference number: Z23031
A/Accession: T6378
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-375 <AAA>
A/Cross-references: EMBL:AL137725
A/Experimental source: adult testis; clone DKFZp434G0719
C/Genetics:
A/Note: DKFZp434G0719.1

Query Match 2.3%; Score 7; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 266 AYRRGYF 272
Db 317 AYRRGYF 323

RESULT 44

F71815
hypothetical protein jhp1379 - Helicobacter pylori (strain J99)
C/Species: Helicobacter pylori
A/Variety: strain J99
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C/Accession: F71815
R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Millie, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A/Reference number: A71800; MUID:99120557; PMID:9923682
A/Accession: F71815
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-376 <ARN>
A/Cross-references: GB:AE001560; GB:AE001439; NID:94155981; PIDN:AA006950.1; PID:9415598
A/Experimental source: strain J99
C/Genetics:
A/Gene: jhp1379
C/Superfamily: conserved hypothetical integral membrane protein HP1486

Query Match 2.3%; Score 7; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 LRLCARL 15
Db 220 LRLCARL 226

RESULT 45

E88421
protein R74.2 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: E88421
R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: E88421

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-380 <STO>
A/Cross-references: GB:chr III; PIDN:CA85275.1; PID:31879161; GSPDB:GN00021; CESP:R74.2
A/Note: Second exon possesses a glycine rich domain
C/Genetics:
A/Gene: R74.2
A/Map position: 3

Query Match 2.3%; Score 7; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 266 AYRRGYF 272
Db 115 AYRRGYF 121

RESULT 46

T24963
hypothetical protein T18D3.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T24963
R/Murray, A.
submitted to the EMBL Data Library, November 1995
A/Reference number: Z19962
A/Accession: T24963
A/Status: preliminary; translated from GB/EMBL/DDBU
A/Molecule type: DNA
A/Residues: 1-382 <WIL>
A/Cross-references: EMBL:Z68119; PIDN:CAA92193.1; GSPDB:GN00028; CESP:T18D3.3
A/Experimental source: clone T18D3
C/Genetics:
A/Gene: CESP:T18D3.3
A/Map position: X
A/Introns: 34/2; 72/1; 142/1; 193/2; 254/3; 290/1; 325/3

Query Match 2.3%; Score 7; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 248 GVLVWLA 254
Db 158 GVLVWLA 164

RESULT 47

E72539
hypothetical protein APE1602 - Aeropyrum pernix (strain KI)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C/Accession: E72539
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: E72539
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-391 <KAM>
A/Cross-references: DBU:AP000062; NID:95105244; PIDN:BAA80602.1; PID:d1044388; PID:9510
A/Experimental source: strain KI
C/Genetics:
A/Gene: APE1602

Query Match 2.3%; Score 7; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPPRL 11
 |||||
 DB 64 RPPRL 70

RESULT 48

RHUPD poliovirus receptor splice form delta precursor - human

N.Alternate names: poliovirus receptor H208

C.Species: Homo sapiens (man)

C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997

C.Accession: A43024; B1496

R.Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take

EMBO J. 9, 3217-3224, 1990

A.Title: The poliovirus receptor protein is produced both as membrane-bound and secreted

A.Reference number: S12048; PMID:9106015; PMID:2170108

A.Accession: A43024

A.Molecule type: DNA

A.Residues: 1-392 <KOI>

A.Cross-references: EMBL:X64116

A.Note: 67-Ala was also found

R.Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.

Cell 56, 855-865, 1989

A.Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and c

A.Reference number: A90910; PMID:89168426; PMID:2538245

A.Accession: B1496

A.Molecule type: mRNA

A.Residues: 1-66; 'A', 68-392 <MEN>

A.Cross-references: GB:M24406

C.Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f

C.Genetics:

A.Gene: GDB:PVR; PVS

A.Cross-references: GDB:120324; OMIM:173850

A.Map position: 19q13.2-19q13.2

A.Introns: 27/1; 143/1; 242/1; 281/2; 331/1

C.Superfamily: poliovirus receptor; immunoglobulin homology

C.Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-392/Product: poliovirus receptor delta #status predicted <MAT>

F:21-343/Domain: extracellular #status predicted <EXT>

F:42-125/Domain: immunoglobulin homology <IMM1>

F:159-223/Domain: immunoglobulin homology <IMM2>

F:259-314/Domain: immunoglobulin homology <IMM3>

F:344-367/Domain: transmembrane #status predicted <TMN>

F:368-392/Domain: intracellular #status predicted <INT>

F:49-123, 166-221, 266-312/disulfide bonds: #status predicted

F:105, 120, 188, 218, 237, 278, 307, 313/Binding site: carbohydrate (asn) (covalent) #status pr

Query Match 2.3%; Score 7; DB 1; Length 392;
 Best Local Similarity 100.0%; Pred. No. 82;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ELTVQVK 138
 |||||
 DB 324 ELTVQVK 330

RESULT 49

B44194

poliovirus receptor (clone AGM-delta-1) - green monkey

C.Species: Cercopithecus aethiops (green monkey, grivet)

C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C.Accession: B44194

R.Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotch, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A.Title: A second gene for the African green monkey poliovirus receptor that has no puta

A.Reference number: A44194; PMID:93059651; PMID:1331508

A.Accession: B44194

A.Status: preliminary

A.Molecule type: DNA
 A.Residues: 1-392 <KOI>
 A.Cross-references: GB:S48817
 C.Superfamily: poliovirus receptor; immunoglobulin homology
 F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 2.3%; Score 7; DB 2; Length 392;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ELTVQVK 138
 |||||
 DB 324 ELTVQVK 330

RESULT 50

T24258

hypothetical protein R74.2 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C.Accession: T24258

R.Gardner, A.

submitted to the EMBL Data Library, August 1994

A.Reference number: Z19864

A.Accession: T24258

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-400 <MTI>

A.Cross-references: EMBL:Z36238; PIDN:CA85275.2; GSPDB:GN00021; CESP:R74.2

A.Experimental source: clone R74

C.Genetics:

A.Gene: CESP:R74.2

A.Map position: 3

A.Introns: 45/3; 65/3; 326/2

Query Match 2.3%; Score 7; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 83;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 AYRRGYF 272
 |||||
 DB 135 AYRRGYF 141

Search completed: December 15, 2003, 15:00:57
 Job time : 24 secs